



#9

SEQUENCE LISTING

<110> Agarwal, Poonam
Aizenstein, Brian
Arco, David
Atilles, Myrta
Burris, Deborah
de Arruda Indig, Monika
Law, Scott
Mast, Andrea
Marshall, David
Miller, Carolyn
Oldenberg, Mary
Rasmussen, Eric
Schneiders, Jennifer

<120> Methods and Compositions for Detecting Target Sequences

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<150> 09/381,212

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<150> 08/682,853

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<160> 253

<170> PatentIn version 3.0

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 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
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 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 785 790 795 800
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 Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
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 Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
 65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
 85 90 95
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
 100 105 110
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
 115 120 125
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
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 Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
 145 150 155 160
 Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
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 Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
 180 185 190
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
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 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
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 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
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 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
 260 265 270
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
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 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
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 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
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 325 330 335
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 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
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 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
 405 410 415

Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
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 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
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 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala
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 Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
 485 490 495
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 500 505 510
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 Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr
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 565 570 575
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 595 600 605
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
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 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln
 625 630 635 640
 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu
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 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala
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 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala
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 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
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Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe
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 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp
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 785 790 795 800
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 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
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Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	130	135	140	
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Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	165	170	175	
Glu	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Xaa	Gly	Asp	Pro	Ser	Asp	Asn	180	185	190	
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Xaa	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Val	210	215	220	
Lys	Pro	Xaa	Xaa	Arg	Glu	Lys	Ile	Xaa	Ala	His	Met	Glu	Asp	Leu	Xaa	225	230	235	240
Leu	Ser	Xaa	Xaa	Leu	Ser	Xaa	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	245	250	255	
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 <220>
 <223> Synthetic
 <400> 41
 gcgacactcc accatagat 19
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 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 42
 ctgtcttcac gcagaaagc 19



<210> 43
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<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 43
gcacggtcta cgagacctc 19
<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 44
taatacgact cactataggg 20
<210> 45
<211> 337
<212> RNA
<213> Artificial Sequence
<220>
<223> Synthetic
<400> 45
gggaaagcuu gcaugccugc aggucgacuc uagaggau cu acuagucua uggauucugu 60
cuucacgcag aaagcgucug gccaugggcu uaguaugagu gucgugcagc cuccaggacc 120
ccccucccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aaaugccagg 180
acgaccgggu ccuuucugg auaaaccgc ucaaugccug gagauuugg cgugcccccg 240
caagacugcu agccgaguag uguugggucg cgaaaggccu ugugguacug ccugauaggg 300
ugccugcgag ugccccggga ggucucguag accgugc 337
<210> 46
<211> 19
<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (17)..(17)
 <223> The T at this position is linked to a fluorescein dye on an abasi
 c linker
 <400> 46
 ccggtcgtcc tggcaatcc 19
 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 47
 gtttatccaa gaaaggaccc ggtc 24
 <210> 48
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 48
 caggggtgaag ggaagaagaa agcgaaagg 30
 <210> 49
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 49
 caggggggaag ggaagaagaa agcgaaagg 30

<210> 50
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The T residues at these positions are amino modified T residues.
 <400> 50
 ttcttttcac cagcgagacg gg 22
 <210> 51
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 51
 attgggcgcc aggggtggttt tt 22
 <210> 52
 <211> 53
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 52
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210> 53
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 53
 gaattcgatt taggtgacac tatagaatac a 31
 <210> 54
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 54
 ccttttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42
 <210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 55
 gccggcgaac gtggcgagaa agga 24
 <210> 56
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 56
 cagaaggaag ggaagaaagc gaaagg 26

<210> 57
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 57
 cagggggaag ggaagaaagc gaaagg 26
 <210> 58
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 58
 caggggtacag ggaagaaagc gaaagg 26
 <210> 59
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 59
 gggaaagtcc tcggagccgc gcgggacgag cgtggggggcc cg 42
 <210> 60
 <211> 963
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
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<221> CDS

<222> (1) .. (960)

<400> 60

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Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly	
1 5 10 15	
atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc	96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly	
20 25 30	
cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc	144
His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr	
35 40 45	
agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc	192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu	
50 55 60	
ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac	240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp	
65 70 75 80	
gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg	288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala	
85 90 95	
ggc cgg gcc ccc acg ctc gtc ccg cgc ggc tcc gag gac ttt ccc cgg	336
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg	
100 105 110	
caa ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc	384
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg	
115 120 125	
ctc gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc	432
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala	
130 135 140	
aag aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac	480
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	
145 150 155 160	
aaa gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc	528
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	
165 170 175	
gag ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg	576
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	
180 185 190	
agg ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc	624
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	
195 200 205	
gac aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag	672
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys	
210 215 220	

ctt ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac	720
Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp	
225 230 235 240	
cgg ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat	768
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp	
245 250 255	
ctg aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg	816
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu	
260 265 270	
gag gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg	864
Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg	
275 280 285	
gcc ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc	912
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly	
290 295 300	
ctt ctg gaa agc ccc aag gcc gca ctc gag cac cac cac cac cac	960
Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His	
305 310 315 320	
tga	963

<210> 61

<211> 320

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 61

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser	Gly
1				5					10					15	

Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
			20					25						30	

His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		35					40					45			

Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
	50					55					60				

Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
65					70					75					80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala

	85		90		95
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg	100		105		110
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg	115		120		125
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala	130		135		140
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	145		150		155
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	165		170		175
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	180		185		190
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	195		200		205
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys	210		215		220
Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp	225		230		235
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp	245		250		255
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu	260		265		270
Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg	275		280		285
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly	290		295		300
Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His	305		310		315
					320
<210>	62				
<211>	20				

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 62
 cgatctcctc ggccacctcc 20
 <210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 63
 ggcgggtgccc tggacgggca 20
 <210> 64
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 <223> Synthetic
 <400> 64
 ccagctcggt gtggacctga 20
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 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
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<221> CDS

<222> (1) .. (2499)

<400> 65

atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc	48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu	
1 5 10 15	
ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag	96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	
20 25 30	
ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc	144
Gly Leu Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	
35 40 45	
gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc	192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	
50 55 60	
gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg	240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	
65 70 75 80	
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa	288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	
85 90 95	
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc	336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	
100 105 110	
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	

ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240	720
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255	768
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270	816
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu 275 280 285	864
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu 290 295 300	912
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320	960
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 335	1008
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350	1056
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365	1104
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380	1152
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400	1200
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 415	1248
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430	1296
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445	1344
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460	1392

gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc acg ggc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Gly Arg Leu Ser 565 570 575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gac tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112

cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 66

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 66

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg

545		550		555		560
Leu His Thr Arg	Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser					
	565			570		575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly						
	580			585		590
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val						
	595			600		605
Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser						
	610			615		620
Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His						
	625			630		640
Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp						
				645		655
Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr						
	660			665		670
Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu						
	675			680		685
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val						
	690			695		700
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr						
	705			710		720
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala						
				725		735
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met						
	740			745		750
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys						
	755			760		765
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val						
	770			775		780
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val						
	785			790		800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

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<210> 68

<211> 2505

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Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

48

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

96

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

144

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

192

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg	240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	
65 70 75 80	
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa	288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	
85 90 95	
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc	336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	
100 105 110	
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc ccg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg ccg gag ccc gac ccg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	

ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320	960
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 335	1008
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350	1056
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365	1104
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380	1152
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400	1200
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 415	1248
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430	1296
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445	1344
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460	1392
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584

atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
acc	tac	att	gac	ccc	ttg	cgg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
	545				550					555					560	
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
cag	agg	atc	cgc	cgg	gcc	ttc	atc	gcc	gag	gag	ggg	tgg	cta	ttg	gtg	1824
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
gcc	ctg	gcc	tat	agc	cag	ata	gag	ctc	agg	gtg	ctg	gcc	cac	ctc	tcc	1872
Ala	Leu	Ala	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
	610					615					620					
ggc	gac	gag	aac	ctg	atc	cgg	gtc	ttc	cag	gag	ggg	cgg	gac	atc	cac	1920
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
	625				630					635					640	
acg	gag	acc	gcc	agc	tgg	atg	ttc	ggc	gtc	ccc	cgg	gag	gcc	gtg	gac	1968
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	
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ccc	ctg	atg	cgc	cgg	gcg	gcc	aag	acc	atc	aac	ttc	ggg	gtc	ctc	tac	2016
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	
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ggc	atg	tcg	gcc	cac	cgc	ctc	tcc	cag	gag	cta	gcc	atc	cct	tac	gag	2064
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	
		675					680				685					
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Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	
	690					695					700					
cgg	gcc	tgg	att	gag	aag	acc	ctg	gag	gag	ggc	agg	agg	cgg	ggg	tac	2160
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	
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gtg	gag	acc	ctc	ttc	ggc	cgc	cgc	cgc	tac	gtg	cca	gac	cta	gag	gcc	2208
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	
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cgg	gtg	aag	agc	gtg	cgg	gag	gcg	gcc	gag	cgc	atg	gcc	ttc	aac	atg	2256
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	
			740					745					750			
ccc	gtc	cag	ggc	acc	gcc	gcc	gac	ctc	atg	aag	ctg	gct	atg	gtg	aag	2304
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	
		755					760					765				

ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
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Glu	

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Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350

Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365

Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380

Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415

Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430

Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445

Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460

Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
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Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
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ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag      96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
                20                               25          30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc      144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
                35                               40          45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc      192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
                50                               55          60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg      240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65                               70          75          80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa      288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
                85                               90          95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc      336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
                100                              105          110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag      384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
                115                              120          125

aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa      432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
                130                              135          140

gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag      480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145                              150          155          160

ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg      528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
                165                              170          175

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ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp 180 185 190	576
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu 195 200 205	624
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg 210 215 220	672
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu 225 230 235 240	720
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu 245 250 255	768
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala 260 265 270	816
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ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu 290 295 300	912
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala 305 310 315 320	960
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala 325 330 335	1008
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu 340 345 350	1056
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu 355 360 365	1104
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser 370 375 380	1152
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr 385 390 395 400	1200
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn 405 410 415	1248

ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg 420 425 430	1296
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr 435 440 445	1344
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val 450 455 460	1392
gcc ggg gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly 465 470 475 480	1440
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe 485 490 495	1488
gac gag cta ggg ctt ccc gcc atc ggc aag acg gag aag acc ggc aag Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys 500 505 510	1536
cgc tcc acc agc gcc gcc gtc ctg gag gcc ctc cgc gag gcc cac ccc Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro 515 520 525	1584
atc gtg gag aag atc ctg cag tac cgg gag ctc acc aag ctg aag agc Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser 530 535 540	1632
acc tac att gac ccc ttg ccg gac ctc atc cac ccc agg acg ggc cgc Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg 545 550 555 560	1680
ctc cac acc cgc ttc aac cag acg gcc acg gcc acc ggc agg cta agt Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser 565 570 575	1728
agc tcc gat ccc aac ctc cag aac atc ccc gtc cgc acc ccg ctt ggg Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly 580 585 590	1776
cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gtc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr	2016

660	665	670	
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gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700			2112
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr 705 710 715 720			2160
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 735			2208
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ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val 770 775 780			2352
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val 785 790 795 800			2400
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val 805 810 815			2448
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys 820 825 830			2496
gag tgatag Glu			2505

<210> 71

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 71

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495

Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met

	740		745		750	
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	755		760		765	
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	770		775		780	
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	785		790		795	800
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val		805		810		815
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys		820		825		830

Glu

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 72

gggataccat gggagtgcag tttgg

25

<210> 73

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73

ggtaaatttt tctcgtcgac atccac

27

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<210> 74
<211> 981
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic
<220>
<221> CDS
<222> (1)..(978)
<400> 74
atg gga gtg cag ttt ggt gat ttt att cca aaa aat att atc tcc ttt      48
Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1          5          10          15

gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta      96
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
          20          25          30

tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga     144
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
          35          40          45

aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa     192
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
          50          55          60

acc ata cat ttg tta gag aat gat ata act cca atc tgg gtt ttt gat     240
Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
        65          70          75          80

ggt gag cca cca aag tta aag gag aaa aca agg aaa gtt agg aga gag     288
Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
          85          90          95

atg aaa gag aaa gct gaa ctt aag atg aaa gag gca att aaa aag gag     336
Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
          100          105          110

gat ttt gaa gaa gct gct aag tat gca aag agg gtt agc tat cta act     384
Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
          115          120          125

ccg aaa atg gtt gaa aac tgc aaa tat ttg tta agt ttg atg ggc att     432
Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
          130          135          140

ccg tat gtt gaa gct ccc tct gag gga gag gca caa gca agc tat atg     480
Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
          145          150          155          160

gca aag aag gga gat gtt tgg gca gtt gta agt caa gat tat gat gcc     528
Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
          165          170          175

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ttg tta tat gga gct ccg aga gtt gtt aga aat tta aca act aca aag Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys 180 185 190	576
gag atg cca gaa ctt att gaa tta aat gag gtt tta gag gat tta aga Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg 195 200 205	624
att tct ttg gat gat ttg ata gat ata gcc ata ttt atg gga act gac Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp 210 215 220	672
tat aat cca gga gga gtt aaa gga ata gga ttt aaa agg gct tat gaa Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu 225 230 235 240	720
ttg gtt aga agt ggt gta gct aag gat gtt ttg aaa aaa gag gtt gaa Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu 245 250 255	768
tac tac gat gag att aag agg ata ttt aaa gag cca aag gtt acc gat Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp 260 265 270	816
aac tat tca tta agc cta aaa ttg cca gat aaa gag gga att ata aaa Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys 275 280 285	864
ttc tta gtt gat gaa aat gac ttt aat tat gat agg gtt aaa aag cat Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His 290 295 300	912
gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr 305 310 315 320	960
tta gat gca tgg ttt aaa taa Leu Asp Ala Trp Phe Lys 325	981

<210> 75

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 75

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
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Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
 35 40 45
 Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
 50 55 60
 Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
 85 90 95
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
 100 105 110
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
 115 120 125
 Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
 130 135 140
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
 165 170 175
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
 210 215 220
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
 225 230 235 240
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
 245 250 255
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285

Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320

Leu Asp Ala Trp Phe Lys
 325

<210> 76

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 76

gaggtgatac catgggtgtc c

21

<210> 77

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

gaaactctgc agcgcgtcag

20

<210> 78

<211> 1023

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1)..(1020)

<400> 78

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1 5 10 15	
gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc	96
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile	
20 25 30	
tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg	144
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met	
35 40 45	
gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg	192
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat	240
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa	288
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga	336
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat	384
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att	432
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	
cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg	480
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met	
145 150 155 160	
gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc	528
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser	
165 170 175	
cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga	576
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly	
180 185 190	
aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag	624
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu	
195 200 205	
ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa	672
Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu	
210 215 220	
aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga	720

Lys	Leu	Ile	Glu	Leu	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Pro	Gly		
225					230					235					240		
gga	ata	aag	ggc	ata	ggc	ctt	aaa	aaa	gct	tta	gag	att	gtt	aga	cac		768
Gly	Ile	Lys	Gly	Ile	Gly	Leu	Lys	Lys	Ala	Leu	Glu	Ile	Val	Arg	His		
				245					250					255			
tca	aaa	gat	ccg	cta	gca	aag	ttc	caa	aag	caa	agc	gat	gtg	gat	tta		816
Ser	Lys	Asp	Pro	Leu	Ala	Lys	Phe	Gln	Lys	Gln	Ser	Asp	Val	Asp	Leu		
			260					265					270				
tat	gca	ata	aaa	gag	ttc	ttc	cta	aac	cca	cca	gtc	aca	gat	aac	tac		864
Tyr	Ala	Ile	Lys	Glu	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asn	Tyr		
		275					280					285					
aat	tta	gtg	tgg	aga	gat	ccc	gac	gaa	gag	gga	ata	cta	aag	ttc	tta		912
Asn	Leu	Val	Trp	Arg	Asp	Pro	Asp	Glu	Glu	Gly	Ile	Leu	Lys	Phe	Leu		
		290				295					300						
tgt	gac	gag	cat	gac	ttt	agt	gag	gaa	aga	gta	aag	aat	gga	tta	gag		960
Cys	Asp	Glu	His	Asp	Phe	Ser	Glu	Glu	Arg	Val	Lys	Asn	Gly	Leu	Glu		
305					310					315				320			
agg	ctt	aag	aag	gca	atc	aaa	agt	gga	aaa	caa	tca	acc	ctt	gaa	agt		1008
Arg	Leu	Lys	Lys	Ala	Ile	Lys	Ser	Gly	Lys	Gln	Ser	Thr	Leu	Glu	Ser		
				325				330						335			
tgg	ttc	aag	aga	taa													1023
Trp	Phe	Lys	Arg														
			340														

<210> 79

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 79

Met	Gly	Val	Pro	Ile	Gly	Glu	Ile	Ile	Pro	Arg	Lys	Glu	Ile	Glu	Leu		
1				5					10					15			
Glu	Asn	Leu	Tyr	Gly	Lys	Lys	Ile	Ala	Ile	Asp	Ala	Leu	Asn	Ala	Ile		
		20						25					30				
Tyr	Gln	Phe	Leu	Ser	Thr	Ile	Arg	Gln	Lys	Asp	Gly	Thr	Pro	Leu	Met		
		35					40					45					
Asp	Ser	Lys	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Leu	Phe	Tyr	Arg		
	50					55					60						

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95
 Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
 100 105 110
 Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
 115 120 125
 Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
 130 135 140
 Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
 145 150 155 160
 Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175
 Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190
 Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205
 Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320

Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
325 330 335

Trp Phe Lys Arg
340

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80
gataccatgg gtgtcccaat tgggtg

25

<210> 81

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 81
tcgacgtcga cttatctctt gaaccaactt tcaaggg

37

<210> 82

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 82
agcgagggag aggccaagc

20

<210> 83

<211> 21

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 83
 gcctatgccc tttattcctc c 21
 <210> 84
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 84
 tggtcgctgt ctgctgaaa gcgagacagc gtg 33
 <210> 85
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 85
 tgctctctgg tcgctgtctg aaagacagcg 30
 <210> 86
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label

<400> 86
 agaaaggaag ggaagaaagc gaaagg 26
 <210> 87
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <220>
 <221> modified_base
 <222> (27)..(27)
 <223> The residue at this position is a dideoxycytidine.
 <400> 87
 agaaaggaag ggaagaaagc gaaaggc 27
 <210> 88
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (24)..(24)
 <223> The residue at this position is a dideoxycytidine.
 <400> 88
 gccggcgaac gtggcgagaa aggc 24

<210> 89
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <220>
 <221> modified_base
 <222> (27)..(27)
 <223> The residue at this position is a dideoxycytidine.
 <400> 89
 agaaaggaag ggaagaaagc gaaaggc 27
 <210> 90
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 90
 aaaattcctt tctctttgcc ctttgcttcc 30

<210> 91
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 91
 ggaaagccgg cgaacgtggc gagaaa 26
 <210> 92
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 92
 ggaaagccgg cgaacgtggc gaga 24
 <210> 93
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing Cy3
 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label

<400> 93
 agaaaggaag ggaagaaagc gaaaggt 27
 <210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing Cy3
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions are amine-T.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <223> The residue at this position is linked to a spacer containing a f
 fluorescein label
 <400> 94
 ttccagagcc taatttgcca gta 23
 <210> 95
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> modified_base
 <222> (1)..(1)
 <223> The residue at this position has a 5' TET-label.
 <220>
 <221> misc_feature
 <222> (22)..(22)
 <400> 95
 ttccagagcc taatttgcca gta 23
 <210> 96
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 96
 cttaccaacg ctaacgagcg tcttg 25
 <210> 97
 <211> 43
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 97
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca ata 43
 <210> 98
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 98
 tattgggagc catggtgggt ttt 23

<210> 99
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residue at this position is a 5-nitroindole.
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 5-nitroindole.
 <400> 99
 tattgggcgn cagggngggt ttt
 <210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residue at this position is a 5-nitroindole.
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 5-nitroindole.
 <400> 100
 tattgggcgn catggngggt ttt

23

23

<210> 101
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 3-nitropyrrole group.
 <400> 101
 tattgggcgc cagggngggt ttt 23
 <210> 102
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (16)..(16)
 <223> The residue at this position is a 3-nitropyrrole group.
 <400> 102
 tattgggcgc catggngggt ttt 23
 <210> 103
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference

<222> (1)..(1)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)

<220>
 <221> misc_difference
 <222> (9)..(10)
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thi
 omonophosphate)
 <400> 103
 ctgaatataa acttgtggta gttggagctg gtgccgtagg caagagtgcc ttgacg 56
 <210> 104
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residue at these positions are a 2'deoxyadenosine 5'-O-(1-Thi
 omonophosphate)

<220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residue at this position is a 2'deoxyadenosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(10)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <400> 104
 ctgaatataa acttggtgta gttggagctg gtagcgtagg caagagtgcc ttgacg 56
 <210> 105
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)

<220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(4)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (5)..(6)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(8)
 <223> The residues at these positions are a 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <400> 105
 gctcaaggca ctcttgacct cga

23

<210> 106
 <211> 8
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 amidite label
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions have an amino group added.
 <400> 106
 ttcaccag

8

<210> 107
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon
 ophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)

<220>
 <221> misc_difference
 <222> (3)..(4)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thi
 omonophosphate)
 <220>
 <221> misc_difference
 <222> (5)..(6)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(7)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thi
 omonophosphate)
 <220>
 <221> misc_difference
 <222> (8)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <400> 107
 ctccaactac cacaagttta tattcag 27
 <210> 108
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 108
 cgagagacca cgct 14

<210> 109
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (14)..(14)
 <223> The residue at this position contains an abasic ribose.
 <400> 109
 cgagagacca cgct 14
 <210> 110
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (14)..(14)
 <223> The residue at this position contains an abasic ribose with a 3'
 phosphate group
 <400> 110
 cgagagacca cgct 14
 <210> 111
 <211> 15
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_difference
 <222> (15)..(15)
 <223> The residue at this position contains a 3' phosphate group.
 <400> 111
 cgagagacca cgctg 15
 <210> 112
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (2)..(2)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (3)..(4)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (5)..(5)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)

<220>
 <221> misc_difference
 <222> (6)..(6)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (7)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)
 <400> 112
 gtaatcttac caacgctaac gagcgtcttg 30
 <210> 113
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(2)
 <223> The residues at these positions are a 2'deoxycytosine 5'-O-(1-Thiomonophosphate)

<220>
 <221> misc_difference
 <222> (3)..(3)
 <223> The residue at this position is a 2'deoxythymidine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (4)..(5)
 <223> The residues at these positions are a 2'deoxyadenosine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (6)..(8)
 <223> The residues at these positions are a 2'deoxythymidine 5'-O-(1-Th
 iomonophosphate)
 <220>
 <221> misc_difference
 <222> (9)..(9)
 <223> The residue at this position is a 2'deoxyguanosine 5'-O-(1-Thiomo
 nophosphate)
 <220>
 <221> misc_difference
 <222> (10)..(10)
 <223> The residue at this position is a 2'deoxycytosine 5'-O-(1-Thiomon
 ophosphate)
 <400> 113
 cctaatttgc cagttacaaa ataaacagcc c
 <210> 114
 <211> 8
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

31

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <220>
 <221> modified_base
 <222> (1)..(2)
 <223> The residues at these positions have an amino group added.
 <400> 114
 ttccagag 8
 <210> 115
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 115
 ttttccagag cctaataaaa ttaggctctg gaaagacgct cgtg 44
 <210> 116
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 116
 aacgagcgtc ttg 14
 <210> 117
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 117
 aacgagcgtc attg 14
 <210> 118
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 118
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg 50
 <210> 119
 <211> 17
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 119
 ttttccagag cctaattg 17
 <210> 120
 <211> 13
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position has a TET label.
 <400> 120
 ccggtcgtcc tgg 13

<210> 121
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 121
 caattccggg gtactcacgg gttcc 25
 <210> 122
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position has a TET label.
 <400> 122
 ccggtcgtcc tggcaa 16
 <210> 123
 <211> 47
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 123
 tgttttgacc tccatagaag accctatagt gagtcgtatt aatttcg 47
 <210> 124
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 124

cgaaattaat acgactcact ata

23

<210> 125

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 125

cgaaattaat acgactcact ataccagaa

30

<210> 126

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 126

cgaaattaat acgact

16

<210> 127

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 127

cgaaattaat acg

13

<210> 128
 <211> 12
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 128
 cgaaattaat ac 12
 <210> 129
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 129
 cactataggg tcttctatgg aggtc 25
 <210> 130
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 130
 actcactata gggctcttcta tggaggtc 28
 <210> 131
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 131
 gactcactat agggctcttct atggaggtc 29

<210> 132
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 132
 cgaaattaat acgcagtatg ttagcaaacg 30
 <210> 133
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 133
 gaactggcat gattaagact ccttattacc 30
 <210> 134
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 134
 gaactggcat gattaagact ccttattaa 29
 <210> 135
 <211> 326
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 135

Met	Gly	Val	Gln	Phe	Gly	Asp	Phe	Ile	Pro	Lys	Asn	Ile	Ile	Ser	Phe	1	5	10	15
Glu	Asp	Leu	Lys	Gly	Lys	Lys	Val	Ala	Ile	Asp	Gly	Met	Asn	Ala	Leu	20	25	30	
Tyr	Gln	Phe	Leu	Thr	Ser	Ile	Arg	Leu	Arg	Asp	Gly	Ser	Pro	Leu	Arg	35	40	45	
Asn	Arg	Lys	Gly	Glu	Ile	Thr	Ser	Ala	Tyr	Asn	Gly	Val	Phe	Tyr	Lys	50	55	60	
Thr	Ile	His	Leu	Leu	Glu	Asn	Asp	Ile	Thr	Pro	Ile	Trp	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Lys	Leu	Lys	Glu	Lys	Thr	Arg	Lys	Val	Arg	Arg	Glu	85	90	95	
Met	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Met	Lys	Glu	Ala	Ile	Lys	Lys	Glu	100	105	110	
Asp	Phe	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr	115	120	125	
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile	130	135	140	
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met	145	150	155	160
Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala	165	170	175	
Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys	180	185	190	
Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg	195	200	205	
Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp	210	215	220	
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu	225	230	235	240
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu	245	250	255	
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp	260	265	270	
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys	275	280	285	
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His	290	295	300	

Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320

Leu Asp Ala Trp Phe Lys
 325

<210> 136

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 136

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15

Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30

Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45

Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60

Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
 100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
 115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
 130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
 145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 137

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 137

Met Gly Ile Gln Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser
 1 5 10 15
 Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
 20 25 30
 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35 40 45
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50 55 60
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65 70 75 80
 Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Gln Leu Lys Ser Gly Glu
 85 90 95
 Leu Ala Lys Arg Ser Glu Arg Arg Ala Glu Ala Glu Lys Gln Leu Gln
 100 105 110
 Gln Ala Gln Ala Ala Gly Ala Glu Gln Glu Val Glu Lys Phe Thr Lys
 115 120 125

Arg Leu Val Lys Val Thr Lys Gln His Asn Asp Glu Cys Lys His Leu
 130 135 140
 Leu Ser Leu Met Gly Ile Pro Tyr Leu Asp Ala Pro Ser Glu Ala Glu
 145 150 155 160
 Ala Ser Cys Ala Ala Leu Val Lys Ala Gly Lys Val Tyr Ala Ala Ala
 165 170 175
 Thr Glu Asp Met Asp Cys Leu Thr Phe Gly Ser Pro Val Leu Met Arg
 180 185 190
 His Leu Thr Ala Ser Glu Ala Lys Lys Leu Pro Ile Gln Glu Phe His
 195 200 205
 Leu Ser Arg Ile Leu Gln Glu Leu Gly Leu Asn Gln Glu Gln Phe Val
 210 215 220
 Asp Leu Cys Ile Leu Leu Gly Ser Asp Tyr Cys Glu Ser Ile Arg Gly
 225 230 235 240
 Ile Gly Pro Lys Arg Ala Val Asp Leu Ile Gln Lys His Lys Ser Ile
 245 250 255
 Glu Glu Ile Val Arg Arg Leu Asp Pro Asn Lys Tyr Pro Val Pro Glu
 260 265 270
 Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro Glu Val
 275 280 285
 Leu Asp Pro Glu Ser Val Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu
 290 295 300
 Glu Leu Ile Lys Phe Met Cys Gly Glu Lys Gln Phe Ser Glu Glu Arg
 305 310 315 320
 Ile Arg Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr
 325 330 335
 Gln Gly Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser
 340 345 350
 Ala Lys Arg Lys Glu Pro Glu Pro Lys Gly Ser Thr Lys Lys Lys Ala
 355 360 365
 Lys Thr Gly Ala Ala Gly Lys Phe Lys Arg Gly Lys
 370 375 380

<210> 138

<211> 378

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 138

Met	Gly	Ile	His	Gly	Leu	Ala	Lys	Leu	Ile	Ala	Asp	Val	Ala	Pro	Ser	1	5	10	15
Ala	Ile	Arg	Glu	Asn	Asp	Ile	Lys	Ser	Tyr	Phe	Gly	Arg	Lys	Val	Ala	20	25	30	
Ile	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Ala	Val	Arg	Gln	35	40	45	
Gly	Gly	Asp	Val	Leu	Gln	Asn	Glu	Glu	Gly	Glu	Thr	Thr	Ser	Leu	Met	50	55	60	
Gly	Met	Phe	Tyr	Arg	Thr	Ile	Arg	Met	Glu	Asn	Gly	Ile	Lys	Pro	Val	65	70	75	80
Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	Leu	Ala	85	90	95	
Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	Gln	Ala	100	105	110	
Gln	Glu	Ala	Gly	Met	Glu	Glu	Glu	Val	Glu	Lys	Phe	Thr	Lys	Arg	Leu	115	120	125	
Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu	Leu	Ser	130	135	140	
Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Ser	145	150	155	160
Cys	Ala	Ala	Leu	Ala	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	Thr	Glu	165	170	175	
Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	His	Leu	180	185	190	
Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	Leu	Ser	195	200	205	
Arg	Val	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	Asp	Leu	210	215	220	
Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	Ile	Gly	225	230	235	240
Ala	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile	Glu	Glu	245	250	255	
Ile	Val	Arg	Arg	Leu	Asp	Pro	Ser	Lys	Tyr	Pro	Val	Pro	Glu	Asn	Trp	260	265	270	
Leu	His	Lys	Glu	Ala	Gln	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	Val	Asp	275	280	285	
Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	Glu	Leu	290	295	300	
Val	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg	Ile	Arg	305	310	315	320

Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly
325 330 335
Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys
340 345 350
Arg Lys Glu Pro Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr
355 360 365
Gly Gly Ala Gly Lys Phe Arg Arg Gly Lys
370 375

<210> 139

<211> 382

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 139

Met Gly Ile Lys Gly Leu Asn Ala Ile Ile Ser Glu His Val Pro Ser
1 5 10 15
Ala Ile Arg Lys Ser Asp Ile Lys Ser Phe Phe Gly Arg Lys Val Ala
20 25 30
Ile Asp Ala Ser Met Ser Leu Tyr Gln Phe Leu Ile Ala Val Arg Gln
35 40 45
Gln Asp Gly Gly Gln Leu Thr Asn Glu Ala Gly Glu Thr Thr Ser His
50 55 60
Leu Met Gly Met Phe Tyr Arg Thr Leu Arg Met Ile Asp Asn Gly Ile
65 70 75 80
Lys Pro Cys Tyr Val Phe Asp Gly Lys Pro Pro Asp Leu Lys Ser His
85 90 95
Glu Leu Thr Lys Arg Ser Ser Arg Arg Val Glu Thr Glu Lys Lys Leu
100 105 110
Ala Glu Ala Thr Thr Glu Leu Glu Lys Met Lys Gln Glu Arg Arg Leu
115 120 125
Val Lys Val Ser Lys Glu His Asn Glu Glu Ala Gln Lys Leu Leu Gly
130 135 140
Leu Met Gly Ile Pro Tyr Ile Ile Ala Pro Thr Glu Ala Glu Ala Gln
145 150 155 160
Cys Ala Glu Leu Ala Lys Lys Gly Lys Val Tyr Ala Ala Ala Ser Glu
165 170 175
Asp Met Asp Thr Leu Cys Tyr Arg Thr Pro Phe Leu Leu Arg His Leu
180 185 190

Thr Phe Ser Glu Ala Lys Lys Glu Pro Ile His Glu Ile Asp Thr Glu
 195 200 205
 Leu Val Leu Arg Gly Leu Asp Leu Thr Ile Glu Gln Phe Val Asp Leu
 210 215 220
 Cys Ile Met Leu Gly Cys Asp Tyr Cys Glu Ser Ile Arg Gly Val Gly
 225 230 235 240
 Pro Val Thr Ala Leu Lys Leu Ile Lys Thr His Gly Ser Ile Glu Lys
 245 250 255
 Ile Val Glu Phe Ile Glu Ser Gly Glu Ser Asn Asn Thr Lys Trp Lys
 260 265 270
 Ile Pro Glu Asp Trp Pro Tyr Lys Gln Ala Arg Met Leu Phe Leu Asp
 275 280 285
 Pro Glu Val Ile Asp Gly Asn Glu Ile Asn Leu Lys Trp Ser Pro Pro
 290 295 300
 Lys Glu Lys Glu Leu Ile Glu Tyr Leu Cys Asp Asp Lys Lys Phe Ser
 305 310 315 320
 Glu Glu Arg Val Lys Ser Gly Ile Ser Arg Leu Lys Lys Gly Leu Lys
 325 330 335
 Ser Gly Ile Gln Gly Arg Leu Asp Gly Phe Phe Gln Val Val Pro Lys
 340 345 350
 Thr Lys Glu Gln Leu Ala Ala Ala Lys Arg Ala Gln Glu Asn Lys
 355 360 365
 Lys Leu Asn Lys Asn Lys Asn Lys Val Thr Lys Gly Arg Arg
 370 375 380

<210> 140

<211> 387

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 140

Met Gly Val His Ser Phe Trp Asp Ile Ala Gly Pro Thr Ala Arg Pro
 1 5 10 15
 Val Arg Leu Glu Ser Leu Glu Asp Lys Arg Met Ala Val Asp Ala Ser
 20 25 30
 Ile Trp Ile Tyr Gln Phe Leu Lys Ala Val Arg Asp Gln Glu Gly Asn
 35 40 45
 Ala Val Lys Asn Ser His Ile Thr Gly Phe Phe Arg Arg Ile Cys Lys
 50 55 60

Leu Leu Tyr Phe Gly Ile Arg Pro Val Phe Val Phe Asp Gly Gly Val
 65 70 75 80
 Pro Val Leu Lys Arg Glu Thr Ile Arg Gln Arg Lys Glu Arg Arg Gln
 85 90 95
 Gly Lys Arg Glu Ser Ala Lys Ser Thr Ala Arg Lys Leu Leu Ala Leu
 100 105 110
 Gln Leu Gln Asn Gly Ser Asn Asp Asn Glu Val Thr Met Asp Met Ile
 115 120 125
 Lys Glu Val Gln Glu Leu Leu Ser Arg Phe Gly Ile Pro Tyr Ile Thr
 130 135 140
 Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Glu Leu Leu Gln Leu Asn
 145 150 155 160
 Leu Val Asp Gly Ile Ile Thr Asp Asp Ser Asp Val Phe Leu Phe Gly
 165 170 175
 Gly Thr Lys Ile Tyr Lys Asn Met Phe His Glu Lys Asn Tyr Val Glu
 180 185 190
 Phe Tyr Asp Ala Glu Ser Ile Leu Lys Leu Leu Gly Leu Asp Arg Lys
 195 200 205
 Asn Met Ile Glu Leu Ala Gln Leu Leu Gly Ser Asp Tyr Thr Asn Gly
 210 215 220
 Leu Lys Gly Met Gly Pro Val Ser Ser Ile Glu Val Ile Ala Glu Phe
 225 230 235 240
 Gly Asn Leu Lys Asn Phe Lys Asp Trp Tyr Asn Asn Gly Gln Phe Asp
 245 250 255
 Lys Arg Lys Gln Glu Thr Glu Asn Lys Phe Glu Lys Asp Leu Arg Lys
 260 265 270
 Lys Leu Val Asn Asn Glu Ile Ile Leu Asp Asp Asp Phe Pro Ser Val
 275 280 285
 Met Val Tyr Asp Ala Tyr Met Arg Pro Glu Val Asp His Asp Thr Thr
 290 295 300
 Pro Phe Val Trp Gly Val Pro Asp Leu Asp Met Leu Arg Ser Phe Met
 305 310 315 320
 Lys Thr Gln Leu Gly Trp Pro His Glu Lys Ser Asp Glu Ile Leu Ile
 325 330 335
 Pro Leu Ile Arg Asp Val Asn Lys Arg Lys Lys Lys Gly Lys Gln Lys
 340 345 350
 Arg Ile Asn Glu Phe Phe Pro Arg Glu Tyr Ile Ser Gly Asp Lys Lys
 355 360 365
 Leu Asn Thr Ser Lys Arg Ile Ser Thr Ala Thr Gly Lys Leu Lys Lys
 370 375 380
 Arg Lys Met
 385

<210> 141

<211> 488

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 141

Met	Gly	Val	Ser	Gly	Leu	Trp	Asn	Ile	Leu	Glu	Pro	Val	Lys	Arg	Pro	
1				5					10					15		
Val	Lys	Leu	Glu	Thr	Leu	Val	Asn	Lys	Arg	Leu	Ala	Ile	Asp	Ala	Ser	
			20					25					30			
Ile	Trp	Ile	Tyr	Gln	Phe	Leu	Lys	Ala	Val	Arg	Asp	Lys	Glu	Gly	Asn	
		35					40					45				
Gln	Leu	Lys	Ser	Ser	His	Val	Val	Gly	Phe	Phe	Arg	Arg	Ile	Cys	Lys	
	50					55					60					
Leu	Leu	Phe	Phe	Gly	Ile	Lys	Pro	Val	Phe	Val	Phe	Asp	Gly	Gly	Ala	
65					70					75					80	
Pro	Ser	Leu	Lys	Arg	Gln	Thr	Ile	Gln	Lys	Arg	Gln	Ala	Arg	Arg	Leu	
				85					90						95	
Asp	Arg	Glu	Glu	Asn	Ala	Thr	Val	Thr	Ala	Asn	Lys	Leu	Leu	Ala	Leu	
			100					105					110			
Gln	Met	Arg	His	Gln	Ala	Met	Leu	Leu	Lys	Arg	Asp	Ala	Asp	Glu	Val	
		115					120					125				
Thr	Gln	Val	Met	Ile	Lys	Glu	Cys	Gln	Glu	Leu	Leu	Arg	Leu	Phe	Gly	
	130					135					140					
Leu	Pro	Tyr	Ile	Val	Ala	Pro	Gln	Glu	Ala	Glu	Ala	Gln	Cys	Ser	Lys	
145					150					155					160	
Leu	Leu	Glu	Leu	Lys	Leu	Val	Asp	Gly	Ile	Val	Thr	Asp	Asp	Ser	Asp	
				165					170					175		
Val	Phe	Leu	Phe	Gly	Gly	Thr	Arg	Val	Tyr	Arg	Asn	Met	Phe	Asn	Gln	
			180					185					190			
Asn	Lys	Phe	Val	Glu	Leu	Tyr	Leu	Met	Asp	Asp	Met	Lys	Arg	Glu	Phe	
		195					200					205				
Asn	Val	Asn	Gln	Met	Asp	Leu	Ile	Lys	Leu	Ala	His	Leu	Leu	Gly	Ser	
	210					215					220					
Asp	Tyr	Thr	Met	Gly	Leu	Ser	Arg	Val	Gly	Pro	Val	Leu	Ala	Leu	Glu	
225					230					235					240	
Ile	Leu	His	Glu	Phe	Pro	Gly	Asp	Thr	Gly	Leu	Phe	Glu	Phe	Lys	Lys	
				245					250					255		

Trp Phe Gln Arg Leu Ser Thr Gly His Ala Ser Lys Asn Asp Val Asn
 260 265 270
 Thr Pro Val Lys Lys Arg Ile Asn Lys Leu Val Gly Lys Ile Ile Leu
 275 280 285
 Pro Ser Glu Phe Pro Asn Pro Leu Val Asp Glu Ala Tyr Leu His Pro
 290 295 300
 Ala Val Asp Asp Ser Lys Gln Ser Phe Gln Trp Gly Ile Pro Asp Leu
 305 310 315 320
 Asp Glu Leu Arg Gln Phe Leu Met Ala Thr Val Gly Trp Ser Lys Gln
 325 330 335
 Arg Thr Asn Glu Val Leu Leu Pro Val Ile Gln Asp Met His Lys Lys
 340 345 350
 Gln Phe Val Gly Thr Gln Ser Asn Leu Thr Gln Phe Phe Glu Gly Gly
 355 360 365
 Asn Thr Asn Val Tyr Ala Pro Arg Val Ala Tyr His Phe Lys Ser Lys
 370 375 380
 Arg Leu Glu Asn Ala Leu Ser Ser Phe Lys Asn Gln Ile Ser Asn Gln
 385 390 395 400
 Ser Pro Met Ser Glu Glu Ile Gln Ala Asp Ala Asp Ala Phe Gly Glu
 405 410 415
 Ser Lys Gly Ser Asp Glu Leu Gln Ser Arg Ile Leu Arg Arg Lys Lys
 420 425 430
 Met Met Ala Ser Lys Asn Ser Ser Asp Ser Asp Ser Asp Ser Glu Asp
 435 440 445
 Asn Phe Leu Ala Ser Leu Thr Pro Lys Thr Asn Ser Ser Ser Ile Ser
 450 455 460
 Ile Glu Asn Leu Pro Arg Lys Thr Lys Leu Ser Thr Ser Leu Leu Lys
 465 470 475 480
 Lys Pro Ser Lys Arg Arg Arg Lys
 485

<210> 142

<211> 550

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 142

Met	Gly	Val	Gln	Gly	Leu	Trp	Lys	Leu	Leu	Glu	Cys	Ser	Gly	Arg	Gln	
1				5					10					15		
Val	Ser	Pro	Glu	Ala	Leu	Glu	Gly	Lys	Ile	Leu	Ala	Val	Asp	Ile	Ser	
			20					25					30			
Ile	Trp	Leu	Asn	Gln	Ala	Leu	Lys	Gly	Val	Arg	Asp	Arg	His	Gly	Asn	
		35					40					45				
Ser	Ile	Glu	Asn	Pro	His	Leu	Leu	Thr	Leu	Phe	His	Arg	Leu	Cys	Lys	
	50					55					60					
Leu	Leu	Phe	Phe	Arg	Ile	Arg	Pro	Ile	Phe	Val	Phe	Asp	Gly	Asp	Ala	
65					70					75					80	
Pro	Leu	Leu	Lys	Lys	Gln	Thr	Leu	Val	Lys	Arg	Arg	Gln	Arg	Lys	Asp	
				85					90					95		
Leu	Ala	Ser	Ser	Asp	Ser	Arg	Lys	Thr	Thr	Glu	Lys	Leu	Leu	Lys	Thr	
			100					105					110			
Phe	Leu	Lys	Arg	Gln	Ala	Ile	Lys	Thr	Glu	Arg	Ile	Ala	Ala	Thr	Val	
		115					120					125				
Thr	Gly	Gln	Met	Phe	Leu	Glu	Ser	Gln	Glu	Leu	Leu	Arg	Leu	Phe	Gly	
	130					135					140					
Ile	Pro	Tyr	Ile	Gln	Ala	Pro	Met	Glu	Ala	Glu	Ala	Gln	Cys	Ala	Ile	
145					150					155					160	
Leu	Asp	Leu	Thr	Asp	Gln	Thr	Ser	Gly	Thr	Ile	Thr	Asp	Asp	Ser	Asp	
				165					170					175		
Ile	Trp	Leu	Phe	Gly	Ala	Arg	His	Val	Tyr	Arg	Asn	Phe	Phe	Asn	Lys	
			180					185					190			
Asn	Lys	Phe	Val	Glu	Tyr	Tyr	Gln	Tyr	Val	Asp	Phe	His	Asn	Gln	Leu	
		195					200					205				
Gly	Leu	Asp	Arg	Asn	Lys	Leu	Ile	Asn	Leu	Ala	Tyr	Leu	Leu	Gly	Ser	
	210					215					220					
Asp	Tyr	Thr	Glu	Gly	Ile	Pro	Thr	Val	Gly	Cys	Val	Thr	Ala	Met	Glu	
225					230					235					240	
Ile	Leu	Asn	Glu	Phe	Pro	Gly	His	Gly	Leu	Glu	Pro	Leu	Leu	Lys	Phe	
				245					250					255		
Ser	Glu	Trp	Trp	His	Glu	Ala	Gln	Lys	Asn	Pro	Lys	Ile	Arg	Pro	Asn	
			260					265					270			
Pro	His	Asp	Thr	Lys	Val	Lys	Lys	Lys	Leu	Arg	Thr	Leu	Gln	Leu	Thr	
		275					280					285				
Pro	Gly	Phe	Pro	Asn	Pro	Ala	Val	Ala	Glu	Ala	Tyr	Leu	Lys	Pro	Val	
	290					295					300					
Val	Asp	Asp	Ser	Lys	Gly	Ser	Phe	Leu	Trp	Gly	Lys	Pro	Asp	Leu	Asp	
305					310					315					320	

<400> 143

Met	Gly	Val	Gln	Gly	Leu	Trp	Lys	Leu	Leu	Glu	Cys	Ser	Gly	His	Arg	1	5	10	15
Val	Ser	Pro	Glu	Ala	Leu	Glu	Gly	Lys	Val	Leu	Ala	Val	Asp	Ile	Ser	20	25	30	
Ile	Trp	Leu	Asn	Gln	Ala	Leu	Lys	Gly	Val	Arg	Asp	Ser	His	Gly	Asn	35	40	45	
Val	Ile	Glu	Asn	Ala	His	Leu	Leu	Thr	Leu	Phe	His	Arg	Leu	Cys	Lys	50	55	60	
Leu	Leu	Phe	Phe	Arg	Ile	Arg	Pro	Ile	Phe	Val	Phe	Asp	Gly	Asp	Ala	65	70	75	80
Pro	Leu	Leu	Lys	Lys	Gln	Thr	Leu	Ala	Lys	Arg	Arg	Gln	Arg	Lys	Asp	85	90	95	
Ser	Ala	Ser	Ile	Asp	Ser	Arg	Lys	Thr	Thr	Glu	Lys	Leu	Leu	Lys	Thr	100	105	110	
Phe	Leu	Lys	Arg	Gln	Ala	Leu	Lys	Thr	Asp	Arg	Ile	Ala	Ala	Ser	Val	115	120	125	
Thr	Gly	Gln	Met	Phe	Leu	Glu	Ser	Gln	Glu	Leu	Leu	Arg	Leu	Phe	Gly	130	135	140	
Val	Pro	Tyr	Ile	Gln	Ala	Pro	Met	Glu	Ala	Glu	Ala	Gln	Cys	Ala	Val	145	150	155	160
Leu	Asp	Leu	Ser	Asp	Gln	Thr	Ser	Gly	Thr	Ile	Thr	Asp	Asp	Ser	Asp	165	170	175	
Ile	Trp	Leu	Phe	Gly	Ala	Arg	His	Val	Tyr	Lys	Asn	Phe	Phe	Asn	Lys	180	185	190	
Asn	Lys	Phe	Val	Glu	Tyr	Tyr	Gln	Tyr	Val	Asp	Phe	Tyr	Ser	Gln	Leu	195	200	205	
Gly	Leu	Asp	Arg	Asn	Lys	Leu	Ile	Asn	Leu	Ala	Tyr	Leu	Leu	Gly	Ser	210	215	220	
Asp	Tyr	Thr	Glu	Gly	Ile	Pro	Thr	Val	Gly	Cys	Val	Thr	Ala	Met	Glu	225	230	235	240
Ile	Leu	Asn	Glu	Phe	Pro	Gly	Arg	Gly	Leu	Asp	Pro	Leu	Leu	Lys	Phe	245	250	255	
Ser	Glu	Trp	Trp	His	Glu	Ala	Gln	Asn	Asn	Lys	Lys	Val	Ala	Glu	Asn	260	265	270	
Pro	Tyr	Asp	Thr	Lys	Val	Lys	Lys	Lys	Leu	Arg	Lys	Leu	Gln	Leu	Thr	275	280	285	
Pro	Gly	Phe	Pro	Asn	Pro	Ala	Val	Ala	Asp	Ala	Tyr	Leu	Arg	Pro	Val	290	295	300	
Val	Asp	Asp	Ser	Arg	Gly	Ser	Phe	Leu	Trp	Gly	Lys	Pro	Asp	Val	Asp	305	310	315	320

Ile Trp Leu Asn Gln Ala Val Lys Gly Ala Arg Asp Arg Gln Gly Asn
 35 40 45
 Ala Ile Gln Asn Ala His Leu Leu Thr Leu Phe His Arg Leu Cys Lys
 50 55 60
 Leu Leu Phe Phe Arg Ile Arg Pro Ile Phe Val Phe Asp Gly Glu Ala
 65 70 75 80
 Pro Leu Leu Lys Arg Gln Thr Leu Ala Lys Arg Arg Gln Arg Thr Asp
 85 90 95
 Lys Ala Ser Asn Asp Ala Arg Lys Thr Asn Glu Lys Leu Leu Arg Thr
 100 105 110
 Phe Leu Lys Arg Gln Ala Ile Lys Ala Glu Arg Ile Ala Ala Thr Val
 115 120 125
 Thr Gly Gln Met Cys Leu Glu Ser Gln Glu Leu Leu Gln Leu Phe Gly
 130 135 140
 Ile Pro Tyr Ile Val Ala Pro Met Glu Ala Glu Ala Gln Cys Ala Ile
 145 150 155 160
 Leu Asp Leu Thr Asp Gln Thr Ser Gly Thr Ile Thr Asp Asp Ser Asp
 165 170 175
 Ile Trp Leu Phe Gly Ala Arg His Val Tyr Lys Asn Phe Phe Ser Gln
 180 185 190
 Asn Lys His Val Glu Tyr Tyr Gln Tyr Ala Asp Ile His Asn Gln Leu
 195 200 205
 Gly Leu Asp Arg Ser Lys Leu Ile Asn Leu Ala Tyr Leu Leu Gly Ser
 210 215 220
 Asp Tyr Thr Glu Gly Ile Pro Thr Val Gly Tyr Val Ser Ala Met Glu
 225 230 235 240
 Ile Leu Asn Glu Phe Pro Gly Gln Gly Leu Glu Pro Leu Val Lys Phe
 245 250 255
 Lys Glu Trp Trp Ser Glu Ala Gln Lys Asp Lys Lys Met Arg Pro Asn
 260 265 270
 Pro Asn Asp Thr Lys Val Lys Lys Lys Leu Arg Leu Leu Asp Leu Gln
 275 280 285
 Gln Ser Phe Pro Asn Pro Ala Val Ala Ser Ala Tyr Leu Lys Pro Val
 290 295 300
 Val Asp Glu Ser Lys Ser Ala Phe Ser Trp Gly Arg Pro Asp Leu Glu
 305 310 315 320
 Gln Ile Arg Glu Phe Cys Glu Ser Arg Phe Gly Trp Tyr Arg Leu Lys
 325 330 335
 Thr Asp Glu Val Leu Leu Pro Val Leu Lys Gln Leu Asn Ala Gln Gln
 340 345 350
 Thr Gln Leu Arg Ile Asp Ser Phe Phe Arg Leu Glu Gln His Glu Ala
 355 360 365

Ala Gly Leu Lys Ser Gln Arg Leu Arg Arg Ala Val Thr Cys Met Lys
 370 375 380
 Arg Lys Glu Arg Asp Val Glu Ala Glu Glu Val Glu Ala Ala Val Ala
 385 390 395 400
 Val Met Glu Arg Glu Cys Thr Asn Gln Arg Lys Gly Gln Lys Thr Asn
 405 410 415
 Thr Lys Ser Gln Gly Thr Lys Arg Arg Lys Pro Thr Glu Cys Ser Gln
 420 425 430
 Glu Asp Gln Asp Pro Gly Gly Gly Phe Ile Gly Ile Glu Leu Lys Thr
 435 440 445
 Leu Ser Ser Lys Ala Tyr Ser Ser Asp Gly Ser Ser Ser Asp Ala Glu
 450 455 460
 Asp Leu Pro Ser Gly Leu Ile Asp Lys Gln Ser Gln Ser Gly Ile Val
 465 470 475 480
 Gly Arg Gln Lys Ala Ser Asn Lys Val Glu Ser Ser Ser Ser Ser Asp
 485 490 495
 Asp Glu Asp Arg Thr Val Met Val Thr Ala Lys Pro Val Phe Gln Gly
 500 505 510
 Lys Lys Thr Lys Ser Lys Thr Met Lys Glu Thr Val Lys Arg Lys
 515 520 525
 <210> 145
 <211> 434
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 145
 Met Thr Ile Asn Gly Ile Trp Glu Trp Ala Asn His Val Val Arg Lys
 1 5 10 15
 Val Pro Asn Glu Thr Met Arg Asp Lys Thr Leu Ser Ile Asp Gly His
 20 25 30
 Ile Trp Leu Tyr Glu Ser Leu Lys Gly Cys Glu Ala His His Gln Gln
 35 40 45
 Thr Pro Asn Ser Tyr Leu Val Thr Phe Phe Thr Arg Ile Gln Arg Leu
 50 55 60
 Leu Glu Leu Lys Ile Ile Pro Ile Val Val Phe Asp Asn Ile Asn Ala
 65 70 75 80
 Ser Ser Ser Ala His Glu Ser Lys Asp Gln Asn Glu Phe Val Pro Arg
 85 90 95

Lys	Arg	Arg	Ser	Phe	Gly	Asp	Ser	Pro	Phe	Thr	Asn	Leu	Val	Asp	His	100	105	110
Val	Tyr	Lys	Thr	Asn	Ala	Leu	Leu	Thr	Glu	Leu	Gly	Ile	Lys	Val	Ile	115	120	125
Ile	Ala	Pro	Gly	Asp	Gly	Glu	Ala	Gln	Cys	Ala	Arg	Leu	Glu	Asp	Leu	130	135	140
Gly	Val	Thr	Ser	Gly	Cys	Ile	Thr	Thr	Asp	Phe	Asp	Tyr	Phe	Leu	Phe	145	150	155
Gly	Gly	Lys	Asn	Leu	Tyr	Arg	Phe	Asp	Phe	Thr	Ala	Gly	Thr	Ser	Ser	165	170	175
Thr	Ala	Cys	Leu	His	Asp	Ile	Met	His	Leu	Ser	Leu	Gly	Arg	Met	Phe	180	185	190
Met	Glu	Lys	Lys	Val	Ser	Arg	Pro	His	Leu	Ile	Ser	Thr	Ala	Ile	Leu	195	200	205
Leu	Gly	Cys	Asp	Tyr	Phe	Gln	Arg	Gly	Val	Gln	Asn	Ile	Gly	Ile	Val	210	215	220
Ser	Val	Phe	Asp	Ile	Leu	Gly	Glu	Phe	Gly	Asp	Asp	Gly	Asn	Glu	Glu	225	230	235
Ile	Asp	Pro	His	Val	Ile	Leu	Asp	Arg	Phe	Ala	Ser	Tyr	Val	Arg	Glu	245	250	255
Glu	Ile	Pro	Ala	Arg	Ser	Glu	Asp	Thr	Gln	Arg	Lys	Leu	Arg	Leu	Arg	260	265	270
Arg	Lys	Lys	Tyr	Asn	Phe	Pro	Val	Gly	Phe	Pro	Asn	Cys	Asp	Ala	Val	275	280	285
His	Asn	Ala	Ile	Thr	Met	Tyr	Leu	Arg	Pro	Pro	Val	Ser	Ser	Glu	Ile	290	295	300
Pro	Lys	Ile	Ile	Pro	Arg	Ala	Ala	Asn	Phe	Gln	Gln	Val	Ala	Glu	Ile	305	310	315
Met	Met	Lys	Glu	Cys	Gly	Trp	Pro	Ala	Thr	Arg	Thr	Gln	Lys	Glu	Leu	325	330	335
Ala	Leu	Ser	Ile	Arg	Arg	Lys	Val	His	Leu	Thr	Thr	Thr	Val	Ala	Gln	340	345	350
Thr	Arg	Ile	Pro	Asp	Phe	Phe	Ala	Ala	Thr	Lys	Ser	Lys	Asn	Phe	Thr	355	360	365
Pro	Ile	Val	Glu	Pro	Cys	Glu	Ser	Leu	Glu	Asp	Tyr	Ile	Ser	Ala	Asn	370	375	380
Asn	Thr	Trp	Met	Arg	Lys	Arg	Lys	Arg	Ser	Glu	Ser	Pro	Gln	Ile	Leu	385	390	395

Gln His His Ala Lys Arg Gln Val Pro Asp Arg Lys Arg Ser Val Lys
405 410 415

Ile Arg Ala Phe Lys Pro Tyr Pro Thr Asp Val Ile Glu Leu Gly Asp
420 425 430

Ser Asp

<210> 146

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 146
tactgactca ctatagggtc ttctatggag gtc

33

<210> 147

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 147
ttttttttta attaggctct ggaagacgct gaaagcgtct tg

42

<210> 148

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 148
ttttttttta attaggctct ggaagacgga acgtcttg

38

<210> 149

<211> 34

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 149
 ttttttttta attaggctct ggaagagaat cttg 34
 <210> 150
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 150
 ttttttttta attaggctct ggaaggaact tg 32
 <210> 151
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 151
 ttttttttta attaggctct ggaag 25
 <210> 152
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position has a TET label.
 <400> 152
 attagaaagg aagggaagaa agcgaa 26

<210> 153
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 153
 acgggggaaag ccggcgaacg tggcgagaaa 30
 <210> 154
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 154
 tgacggggaa agccggcgaa cgtggcgaga 30
 <210> 155
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 155
 cttgacgggg aaagccggcg aacgtggcga 30
 <210> 156
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 156
 gcttgacggg gaaagccggc gaacgtggcg 30

<210> 157
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 157
 agaaaggaag ggaagaaa 18
 <210> 158
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference
 <222> (1)..(1)
 <223> The residue at this position contains a fluorescein label.
 <400> 158
 tggaggtcaa aacatcgata agtcgaagaa aggaaggga gaaat 45
 <210> 159
 <211> 14
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_difference

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 159
tgttttgacc tcca 14

<210> 160

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 160
acacagtgtc ctcccgtcc tcctgagcaa 30

<210> 161

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> misc_difference

<222> (1)..(1)

<223> The residue at this position contains a fluorescein label.

<400> 161
tttcctcct cctcttcc 18

<210> 162

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 162
atgaggaaga ggaggagggt gctcaggagg agcgggagga cactgtgtct gtca 54

<210> 163
 <211> 53
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 163
 ttcgctttct tcccttcctt tctcgccacg ttcgccggct ttccccgtca agc 53
 <210> 164
 <211> 1011
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 164
 atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
 ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
 cagcctgacg gtacgcogtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
 atcctataca gagtctccaa catggctgag gtgggaatca ggccggtggt tgtattcgac 240
 ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300
 gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
 caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac 420
 atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
 gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
 ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600
 tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctgggtttg 660
 acgagggagc agctcatcga catagcgatt ctggtcggga cggactacaa tgaggggtgtg 720
 aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
 gcaactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840
 aatcctctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggccttgag 960
 aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttctg a 1011

<210> 165

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

Met	Gly	Ala	Asp	Ile	Gly	Asp	Leu	Phe	Glu	Arg	Glu	Glu	Val	Glu	Leu	
1				5				10					15			
Glu	Tyr	Phe	Ser	Gly	Lys	Lys	Ile	Ala	Val	Asp	Ala	Phe	Asn	Thr	Leu	
			20					25					30			
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	
		35					40					45				
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	
	50					55					60					
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	
65					70				75						80	
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	
				85					90					95		
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	
		100						105					110			
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	
		115					120					125				
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	
	130					135					140					
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	
145					150				155						160	
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	
			165						170					175		
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	
		180						185					190			
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	
		195				200						205				
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	
	210					215					220					
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Glu	Gly	Val	
225					230					235					240	
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	
			245						250					255		

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 166

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166

ccgtcaacat ttaccatggg tgcgga

26

<210> 167

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 167

ccgccacctc gtagtcgaca tccttttcgt g

31

<210> 168

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 168

ggcgaccaca cccgtcctgt

20

<210> 169
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 169
 ccacgatgcg tccggcgtag 20
 <210> 170
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (29)..(29)
 <223> The residue at this position is a 3' amine.
 <400> 170
 aacgaggcgc acccacccaa ggcacagcn 29
 <210> 171
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 171
 acgggtcaat gtccatgccc caaaga 26
 <210> 172
 <211> 28
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (23)..(27)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (28)..(28)
 <223> The residue at this position is a 3' amine.
 <400> 172
 gtctgagatg aaagtgcgcc tcgttaan 28
 <210> 173
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 173
 tcttcgcaca tttcatctca gacgga 26
 <210> 174
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> The residues at these positions are 2'-O-methyls.
 <220>

)

<221> modified_base

<222> (22)..(22)

<223> The residue at this position is a 3' amine.

<400> 174
gctgtgcctt gggtgggtgc gn 22

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified_base

<222> (29)..(29)

<223> The residue at this position is a 3' amine.

<400> 175
aacgaggcgc acccacccaa ggcacagcn 29

<210> 176

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 176
acgggtcaat gtccatgccc caaaga 26

<210> 177

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> modified_base
 <222> (23)..(27)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (28)..(28)
 <223> The residue at this position is a 3' amine.
 <400> 177
 gtctgagatg aaagtgcgcc tcgttaan 28
 <210> 178
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label
 <400> 178
 tcttcgcaca tttcatctca gac 23
 <210> 179
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(17)
 <223> The residues at these positions are 2'-O-methyls.

<220>
 <221> modified_base
 <222> (18)..(18)
 <223> The residue at this position is a 3' amine.
 <400> 179
 gctgtgcctt ggggtgggn

18

<210> 180
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(19)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (20)..(20)
 <223> The residue at this position is a 3' amine.
 <400> 180
 gctgtgcctt ggggtgggtgn

20

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(21)
 <223> The residues at these positions are 2'-O-methyls.

<220>
 <221> modified_base
 <222> (22)..(22)
 <223> The residue at this position is a 3' amine.
 <400> 181
 gctgtgcctt ggggtgggtgc gn 22
 <210> 182
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(22)
 <223> The residues at these positions are 2'-O-methyls.
 <220>
 <221> modified_base
 <222> (23)..(23)
 <223> The residue at this position is a 3' amine.
 <400> 182
 gctgtgcctt ggggtgggtgc gcn 23
 <210> 183
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (1)..(1)
 <223> The residue at this position is linked to a spacer containing a f
 luorescein label

<220>
 <221> modified_base
 <222> (22)..(22)
 <223> The residue at this position indicates 2'-O-methyl sugar.
 <220>
 <221> modified_base
 <222> (42)..(42)
 <223> The residue at this position is a 3' amine.
 <400> 183
 gtctgagatg aaagtgctcc cgcacccacc caaggcacag cn 42
 <210> 184
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(17)
 <223> The residues at these positions are 2'-O-methyl sugars.
 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> The residue at this position is a 3' amine.
 <400> 184
 gctgtgcctt gggtgggn 18
 <210> 185
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_difference
 <222> (29)..(29)
 <223> The residue at this position is a 3' primer.

<400> 185
 aacgaggcgc acccacccaa ggcacagcn 29
 <210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 186
 gctgtgcctt gggtaggtgc g 21
 <210> 187
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.

<400> 187
 gctgtgcctt gggtaggtgc n 21
 <210> 188
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> modified_base
 <222> (15)..(20)
 <223> The residues at these positions are 2'-O-methyl sugars.
 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.
 <400> 188
 gctgtgcctt gggtgggtgc n 21
 <210> 189
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> modified_base
 <222> (1)..(20)
 <223> The residues at these positions are 2'-O-methyl sugars.
 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> The residue at this position is a 3' amine.
 <400> 189
 gctgtgcctt gggtgggtgc n 21
 <210> 190
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> The residue at this position is linked to a spacer containing a fluorescein label

<400> 190
tcttcgcaca ttcatctca gacgga 26

<210> 191

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 191
ctgggcgcgg acatggagga cgtgcgcggc cgcttggtgc agtaccgcgg cgag 54

<210> 192

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 192
ctgggcgcgg acatggagga cgtgtgcggc cgcttggtgc agtaccgcgg cgag 54

<210> 193

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 193
cgcgatgccg atgacctgca gaagcgctg gcagtgtacc aggcgggggc ccgcga 56

<210> 194
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 194
 cgcgatgccg atgacctgca gaagtgcctg gcagtgtacc aggccggggc ccgcga 56
 <210> 195
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> cggtactgcaccaggcgccgct
 <400> 195
 cggtactgca ccaggcggcc gct 23
 <210> 196
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 196
 ccccggcctg gtacactgcc aggct 25
 <210> 197
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 197
 aacgaggcgc acgcacgtcc tccatgt 27

<210> 198
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (24)..(24)
 <223> The residue at this position is linked to 2-amino deoxyadenosine.
 <400> 198
 gaacgaggcg cacacacgtc ctcttgt 27
 <210> 199
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 199
 aacgaggcgc acgcttctgc aggtcatc 28
 <210> 200
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (20)..(20)
 <223> The residue at this position is linked to 2-amino deoxyadenosine.
 <400> 200
 aacgaggcgc acacttctgc gggtcatc 27

<210> 201
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 201
 cctcgtctcg gttttccgag acgaggggtgc gcctcgttc 39
 <210> 202
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 202
 ccctgggga agagcagaga tatacgtc 28
 <210> 203
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 203
 gggctccaca cggcgactct catt 24

<210> 204
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 204
 ggtgctccac ctggcacgta tatctctgct cttccccag 39
 <210> 205
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 205
 ggtgctccac ctggtacgta tatctctgct cttccccag 39
 <210> 206
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 206
 agctgttcgt gttctatgat catgagagtc gccgtgtgga gccccg 46
 <210> 207
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 207
 agctgttcgt gttctatgat gatgagagtc gccgtgtgga gccccg 46

<210> 208
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 208
 aacgaacgcg caggccaggt ggagcattt 29
 <210> 209
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 209
 aacgaacgcg cagaccaggt ggagcac 27
 <210> 210
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 210
 ctccgtctcg gttttccgag acggagctgc gcgttcguuu 40
 <210> 211
 <211> 35
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 211
 aagcacgcag cacgatcata gaacacgaac agttt 35
 <210> 212
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 212
 aagcacgcag caccatcata gaacacgaac agttt 35
 <210> 213
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 213
 acgcgtctcg gttttccgag acgcgtgtgc tgcgtgcuuu 40
 <210> 214
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 214
 gaaggtgtct gcgggagccg atttcatcat cacgcagctt ttctttgagg 50

<210> 215
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 215
 gaaggtgtct gcgggagtcg atttcatcat cacgcagctt ttctttgagg 50
 <210> 216
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 216
 caaagaaaag ctgcgtgatg atgaaatcgc 30
 <210> 217
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 217
 aacgaggcgc acgctcccgc agacac 26
 <210> 218
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 218
 aacgaggcgc acactcccgc agacacc 27

<210> 219
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3 dye
 <400> 219
 cctcgtctcg gttttccgag acgaggggtgc gcctcgttt 39
 <210> 220
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 220
 actgggagca ttgaggctcg ctgagagtca cttttattgg gaaccatagt t 51
 <210> 221
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 221
 actgggagca ttgaggcttg ctgagagtca cttttattgg gaaccatagt t 51

<210> 222
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 222
 tatggttccc aataaaagtg actctcagct 30
 <210> 223
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 223
 aacgaggcgc acgagcctca atgctccc 28
 <210> 224
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 224
 aacgaggcgc acaagcctca atgctccc 28
 <210> 225
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is a spacer bearing a Cy3 dye.
 <400> 225
 cctcgtctcg gttttccgag acgaggggtgc gcctcgttt 39
 <210> 226
 <211> 52
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 226
 tgaagtctag agaaagggtt gtacggctga ggtctggaga aatgggcatc tg 52
 <210> 227
 <211> 46
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 227
 tttgaaatgt cacagggttc ctaacagcca ctcttcctg gatggg 46
 <210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 228
 agatgcccat ttctccagac ctcagccc 28

<210> 229
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 229
 aagcacgcag cacgtacaac cctttctcta gacaaa 36
 <210> 230
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 230
 ctccgtctcg gttttccgag acggaggtgc tgcgtgcuuu 40
 <210> 231
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 231
 ccatccaggg aagagtggcc tgttt 25

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 <220>
 <223> Synthetic
 <400> 232
 aagcacgcag cacaggaacc ctgtgacat 29
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 taggttttga ggggcatggg gacgggggttc agcctccagg gtccta 46
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 taggttttga ggggcatgag gacgggggttc agcctccagg gtccta 46
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 gaccctggag gctgaacccc gtcca 25

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 aacgaggcgc acccatcggg gtcaaaac 28
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 <223> Synthetic
 <400> 237
 aacgaggcgc actcatgccc ctcaaaac 28
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 <223> Synthetic
 <400> 238
 aaggacaaaa tacctgtatt cctcgctgt ccagggatct gctcttacag attaga 56
 <210> 239
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 239
 aaggacaaaa tacctgtatt ccttgctgt ccagggatct gctcttacag attaga 56

<210> 240
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The residue at this position is linked to a purine.
 <400> 240
 taatctgtaa gagcagatcc ctggacagcc 30
 <210> 241
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 241
 aacgaggcgc acgaggaata caggtatattt gtc 33
 <210> 242
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 242
 aacgaggcgc acaaggaata caggtatattt gtc 33

<210> 243
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 243
 ggtaaagggt ggcaaaaaga taac 24
 <210> 244
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 244
 gcgccgaggt cttgggggtgg ttacaag 27
 <210> 245
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <220>
 <221> misc_feature
 <222> (4)..(4)
 <223> The residue at this position is linked to a spacer bearing a Cy3
 dye
 <400> 245
 tctcgtctcg gttttccgag actgagacct cggcgcg 37
 <210> 246
 <211> 29
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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 246

cacttgcttc aggaccatat ttctctctc

29

<210> 247

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 247

cgcgccgagg acaccttttt tagggcgctt tgt

33

<210> 248

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 248

aaaatcgatg gtaaagggtg gc

22

<210> 249

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 249

agttctgcag taccggattt gc

22

<210> 250
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 <213> Artificial Sequence
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 <223> Synthetic
 <400> 250
 tcgctactag ttgcttagtg 20
 <210> 251
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 251
 gtaaacataa gcaactttag 20
 <210> 252
 <211> 41
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 252
 cttgtaacca cccaagatt atctttttgc caacctttac c 41
 <210> 253
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 253
 acaaagcacc ctaaaaaagg tgtagagaga aatatggtcc tgaagcaagt g 51